

SEQUENCE LISTING

<110> Beraud, Christophe
Craven, Andrew
Yu, Ming
Sakowicz, Roman
Patel, Umesh A.
Davies, Katherine A.

<120> NOVEL MOTOR PROTEINS AND METHODS FOR THEIR USE

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<151> 2000-06-15

<160> 6

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<210> 1
<211> 4108
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human kinesin motor protein gene HsKip3a (Figure 1).

<220>
<223> Description of Artificial Sequence: HsKip3a gene.

<400> 1
gccccgcga attcggcacc aggggcgctc tctcccggtg tgggtactgc tgtctgtgg 60
gtggctgtgg gaccctgtgg caagcagcga cgcacggcggc ggagaaccga cgaaagggtgt 120
caccacagtg atggcagtgg aggacagcac gctcaagta gtggtaacggg tgccggccccc 180
caccctcgg gagctggaca gtcagcggcg gccagttttt caggtggtgg acgagcgggt 240
gtctgggtttt aaccctgagg agcccgatgg aggttccctt ggcctgaaat ggggtggcac 300
ccatgtggc cccaaagaaga agggcaaaaga cctgacgtttt gtctttgacc gggctttgg 360
cgaggcggcc acccaacagg acgtgttcca gcacaccacg cacagcgtcc tggacagctt 420
cctccaggcc tacaactgtt cagtgtttgc ctacggggcc accggggctg ggaagacaca 480
caccatgttgg ggaaggggagg gggaccccg catcatgtac ctgaccacccg tggaaactgtt 540
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gcagctgttg gagatactga ccagggggaa ccgttaaccgc acgcagcacc ccactgtatc 780
caacgcgact tcctcccgct cccatgcctt cttccagato tttgtgaagc agcaggacccg 840
ggttccagga ctgacccagg ctgtccaggt ggccaagatg agcctgattt acctggctgg 900
ctcagagcgg gcatccagca cccatgcgaa gggggagcgg ctgcgggagg gggccaaacat 960
caaccgctct ctgctggcgc tcatcaacgt cctcaatgco ttggccgatg caaaggggccg 1020
caagacccat gtgccttacc gggacagcaa actgacccgc ctgctcaaag actccctcg 1080
ggcaactgc cgacagtga tgatcgctgc catcagcccc tccagcctga cctacgagga 1140
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 gggcaccaag cggccacgcgc agtccttcct gcctgccta aggagagggt ctctgcctga 2160
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 tgcgtggatt acaggcgtga gccactgcgc cggcctccc ctctcattta tgcgtccctc 3660
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 cagtccctggt gaagatgtgg atgataatgg tgccttgatt tccaaatgaa gacagcttta 3900
 ttgcattaaactt ctattgtaca taggatacac gttcgttgc taaataaagtg taaaggggaa 3960
 ttcaggctta atgctgcacc tagatataaa tgctaattgat acttgggttt atagccttct 4020
 gatcctttat ttctgcataat atatataat atatacatat attttggta taacaataaa 4080
 ccgtctccat cttggaaa aaaaaaaaaa 4108

<210> 2
 <211> 864
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence encoded by human kinesin motor
 protein gene HsKip3a (Figure 1).

<220>
 <223> Description of Artificial Sequence: Amino acid
 sequence of HsKip3a.

<400> 2
 Met Ala Val Glu Asp Ser Thr Leu Gln Val Val Val Arg Val Arg Pro
 1 5 10 15
 Pro Thr Pro Arg Glu Leu Asp Ser Gln Arg Arg Pro Val Val Gln Val
 20 25 30
 Val Asp Glu Arg Val Leu Val Phe Asn Pro Glu Glu Pro Asp Gly Gly
 35 40 45
 Phe Pro Gly Leu Lys Trp Gly Gly Thr His Asp Gly Pro Lys Lys Lys
 50 55 60
 Gly Lys Asp Leu Thr Phe Val Phe Asp Arg Val Phe Gly Glu Ala Ala
 65 70 75 80
 Thr Gln Gln Asp Val Phe Gln His Thr Thr His Ser Val Leu Asp Ser
 85 90 95
 Phe Leu Gln Gly Tyr Asn Cys Ser Val Phe Ala Tyr Gly Ala Thr Gly
 100 105 110
 Ala Gly Lys Thr His Thr Met Leu Gly Arg Glu Gly Asp Pro Gly Ile
 115 120 125
 Met Tyr Leu Thr Thr Val Glu Leu Tyr Arg Arg Leu Glu Ala Arg Gln
 130 135 140
 Gln Glu Lys His Phe Glu Val Leu Ile Ser Tyr Gln Glu Val Tyr Asn
 145 150 155 160
 Glu Gln Ile His Asp Leu Leu Glu Pro Lys Gly Pro Leu Ala Ile Arg
 165 170 175
 Glu Asp Pro Asp Lys Gly Val Val Val Gln Gly Leu Ser Phe His Gln
 180 185 190
 Pro Ala Ser Ala Glu Gln Leu Leu Glu Ile Leu Thr Arg Gly Asn Arg
 195 200 205
 Asn Arg Thr Gln His Pro Thr Asp Ala Asn Ala Thr Ser Ser Arg Ser
 210 215 220
 His Ala Ile Phe Gln Ile Phe Val Lys Gln Gln Asp Arg Val Pro Gly
 225 230 235 240
 Leu Thr Gln Ala Val Gln Val Ala Lys Met Ser Leu Ile Asp Leu Ala
 245 250 255
 Gly Ser Glu Arg Ala Ser Ser Thr His Ala Lys Gly Glu Arg Leu Arg
 260 265 270
 Glu Gly Ala Asn Ile Asn Arg Ser Leu Leu Ala Leu Ile Asn Val Leu
 275 280 285
 Asn Ala Leu Ala Asp Ala Lys Gly Arg Lys Thr His Val Pro Tyr Arg
 290 295 300
 Asp Ser Lys Leu Thr Arg Leu Leu Lys Asp Ser Leu Gly Gly Asn Cys
 305 310 315 320

Arg Thr Val Met Ile Ala Ala Ile Ser Pro Ser Ser Leu Thr Tyr Glu
 325 330 335

Asp Thr Tyr Asn Thr Leu Lys Tyr Ala Asp Arg Ala Lys Glu Ile Arg
 340 345 350

Leu Ser Leu Lys Ser Asn Val Thr Ser Leu Asp Cys His Ile Ser Gln
 355 360 365

Tyr Ala Thr Ile Cys Gln Gln Leu Gln Ala Glu Val Ala Ala Leu Arg
 370 375 380

Lys Lys Leu Gln Val Tyr Glu Gly Gly Gln Pro Pro Pro Gln Asp
 385 390 395 400

Leu Pro Gly Ser Pro Lys Ser Gly Pro Pro Pro Glu His Leu Pro Ser
 405 410 415

Ser Pro Leu Pro Pro His Pro Pro Ser Gln Pro Cys Thr Pro Glu Leu
 420 425 430

Pro Ala Gly Pro Arg Ala Leu Gln Glu Glu Ser Leu Gly Met Glu Ala
 435 440 445

Gln Val Glu Arg Ala Met Glu Gly Asn Ser Ser Asp Gln Glu Gln Ser
 450 455 460

Pro Glu Asp Glu Asp Glu Gly Pro Ala Glu Glu Val Pro Thr Gln Met
 465 470 475 480

Pro Glu Gln Asn Pro Thr His Ala Leu Pro Glu Ser Pro Arg Leu Thr
 485 490 495

Leu Gln Pro Lys Pro Val Val Gly His Phe Ser Ala Arg Glu Leu Asp
 500 505 510

Gly Asp Arg Ser Lys Gln Leu Ala Leu Lys Val Leu Cys Val Ala Gln
 515 520 525

Arg Gln Tyr Ser Leu Leu Gln Ala Ala Asn Leu Leu Thr Pro Asp Met
 530 535 540

Ile Thr Glu Phe Glu Thr Leu Gln Gln Leu Val Gln Glu Glu Lys Ile
 545 550 555 560

Glu Pro Gly Ala Glu Ala Leu Arg Thr Ser Gly Leu Ala Arg Gly Ala
 565 570 575

Pro Leu Ala Gln Glu Leu Cys Ser Glu Ser Ile Pro Val Pro Ser Pro
 580 585 590

Leu Cys Pro Glu Pro Pro Gly Tyr Thr Gly Pro Val Thr Arg Thr Met
 595 600 605

Ala Arg Arg Leu Ser Gly Pro Leu His Thr Leu Gly Ile Pro Pro Gly
 610 615 620

Pro Asn Cys Thr Pro Ala Gln Gly Ser Arg Trp Pro Met Glu Lys Lys
 625 630 635 640

Arg Arg Arg Pro Ser Ala Leu Glu Ala Asp Ser Pro Met Ala Ser Lys
 645 650 655
 Arg Gly Thr Lys Arg Gln Arg Gln Ser Phe Leu Pro Cys Leu Arg Arg
 660 665 670
 Gly Ser Leu Pro Asp Thr Gln Pro Ser Gln Gly Pro Ser Thr Pro Lys
 675 680 685
 Gly Glu Arg Ala Ser Ser Pro Cys His Ser Pro Arg Val Cys Pro Ala
 690 695 700
 Thr Val Ile Lys Ser Arg Val Pro Leu Gly Pro Ser Ala Met Gln Asn
 705 710 715 720
 Cys Ser Thr Pro Leu Ala Leu Pro Thr Arg Asp Leu Asn Ala Thr Phe
 725 730 735
 Asp Leu Ser Glu Glu Pro Pro Ser Lys Pro Ser Phe His Glu Cys Ile
 740 745 750
 Gly Trp Asp Lys Ile Pro Gln Glu Leu Ser Arg Leu Asp Gln Pro Phe
 755 760 765
 Ile Pro Arg Ala Pro Val Pro Leu Phe Thr Met Lys Gly Pro Lys Pro
 770 775 780
 Thr Ser Ser Leu Pro Gly Thr Ser Ala Cys Lys Lys Lys Arg Val Ala
 785 790 795 800
 Ser Ser Ser Val Ser His Gly Arg Ser Arg Ile Ala Arg Leu Pro Ser
 805 810 815
 Ser Thr Leu Lys Arg Pro Ala Gly Pro Leu Val Leu Pro Glu Leu Pro
 820 825 830
 Leu Ser Pro Leu Cys Pro Ser Asn Arg Arg Asn Gly Lys Asp Leu Ile
 835 840 845
 Arg Val Gly Arg Ala Leu Ser Ala Gly Asn Gly Val Thr Lys Val Ser
 850 855 860

<210> 3
 <211> 1014
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: HsKip3a
 fragment

<220>
 <223> Nucleotide sequence encoding motor domain fragment
 of HsKip3a (Figure 2).

<400> 3
 gacagcacgc tgcaagtgtt ggtacgggtg cggccccc cccctcggta gctggacagt 60

cagcggcggc cagtggttca ggtggtggac gagcgggtgc tggtgtttaa ccctgaggag 120
 cccgatggag ggtccctgg cctgaaatgg ggtggcaccc atgatgccc caagaagaag 180
 ggc当地
 ggtttccaggc acaccacgca cagcgtcctg gacagcttc tccagggcta caactgctca 300
 gttttgcct acggggccac cggggctggg aagacacaca ccatgctggg aagggagggg 360
 gacccggca tcatgtaccc gaccaccgtg gaactgtaca ggcccttga ggcccggccag 420
 caggagaagc acttcgaggt gctcatcagc taccaggagg tgtataatga acagatccat 480
 gaccccttgg agcccaaggg gccccttgc atcccgagg accccgacaa ggggggtggg 540
 gtgcaaggac tttcttcca ccagccagcc tcagccgagc agctgcttga gatactgacc 600
 agggggaaacc gtaaccgcac gcagcacccc actgatgcac acgcgacttc ctcccgctcc 660
 catgcatct tccagatctt tgtgaagcag caggaccggg ttccaggact gacccaggt 720
 gtccagggtgg ccaagatgag cctgattgac ctggctggct cagagccggc atccagcacc 780
 catgcaagg gggagccggc gcggggagggg gccaacatca accgctctt gctggcgctc 840
 atcaacgtcc tcaatgcctt ggccgatgca aaggccgcga agacccatgt gcccctacegg 900
 gacagcaaac tgaccgcct gctcaaagac tccctcgggg gcaactgccc cacagtatg 960
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<210> 4
 <211> 338
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: HsKip3a fragment.

<220>
 <223> Amino acid sequence of the motor domain fragment
 of HsKip3a (Figure 3).

<400> 4
 Asp Ser Thr Leu Gln Val Val Val Arg Val Arg Pro Pro Thr Pro Arg
 1 5 10 15

Glu Leu Asp Ser Gln Arg Arg Pro Val Val Gln Val Val Asp Glu Arg
 20 25 30

Val Leu Val Phe Asn Pro Glu Glu Pro Asp Gly Gly Phe Pro Gly Leu
 35 40 45

Lys Trp Gly Gly Thr His Asp Gly Pro Lys Lys Lys Gly Lys Asp Leu
 50 55 60

Thr Phe Val Phe Asp Arg Val Phe Gly Glu Ala Ala Thr Gln Gln Asp
 65 70 75 80

Val Phe Gln His Thr Thr His Ser Val Leu Asp Ser Phe Leu Gln Gly
 85 90 95

Tyr Asn Cys Ser Val Phe Ala Tyr Gly Ala Thr Gly Ala Gly Lys Thr
 100 105 110

His Thr Met Leu Gly Arg Glu Gly Asp Pro Gly Ile Met Tyr Leu Thr
 115 120 125

Thr Val Glu Leu Tyr Arg Arg Leu Glu Ala Arg Gln Gln Glu Lys His
 130 135 140

Phe Glu Val Leu Ile Ser Tyr Gln Glu Val Tyr Asn Glu Gln Ile His
 145 150 155 160

Asp	Leu	Leu	Glu	Pro	Lys	Gly	Pro	Leu	Ala	Ile	Arg	Glu	Asp	Pro	Asp
165								170					175		
Lys	Gly	Val	Val	Val	Gln	Gly	Leu	Ser	Phe	His	Gln	Pro	Ala	Ser	Ala
180							185					190			
Glu	Gln	Leu	Leu	Glu	Ile	Leu	Thr	Arg	Gly	Asn	Arg	Asn	Arg	Thr	Gln
195							200					205			
His	Pro	Thr	Asp	Ala	Asn	Ala	Thr	Ser	Ser	Arg	Ser	His	Ala	Ile	Phe
210							215					220			
Gln	Ile	Phe	Val	Lys	Gln	Gln	Asp	Arg	Val	Pro	Gly	Leu	Thr	Gln	Ala
225							230					235			240
Val	Gln	Val	Ala	Lys	Met	Ser	Leu	Ile	Asp	Leu	Ala	Gly	Ser	Glu	Arg
245							250					255			
Ala	Ser	Ser	Thr	His	Ala	Lys	Gly	Glu	Arg	Leu	Arg	Glu	Gly	Ala	Asn
260							265					270			
Ile	Asn	Arg	Ser	Leu	Leu	Ala	Leu	Ile	Asn	Val	Leu	Asn	Ala	Leu	Ala
275							280					285			
Asp	Ala	Lys	Gly	Arg	Lys	Thr	His	Val	Pro	Tyr	Arg	Asp	Ser	Lys	Leu
290							295					300			
Thr	Arg	Leu	Leu	Lys	Asp	Ser	Leu	Gly	Gly	Asn	Cys	Arg	Thr	Val	Met
305							310					315			320
Ile	Ala	Ala	Ile	Ser	Pro	Ser	Ser	Leu	Thr	Tyr	Glu	Asp	Thr	Tyr	Asn
325							330					335			

Thr Leu

<210> 5
<211> 383
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: HsKip3a
fragment

<220>
<223> Amino acid sequence of HsKip3a fragment used in
the ATPase assay (Figure 4).

<400> 5
Met Ala Val Glu Asp Ser Thr Leu Gln Val Val Val Arg Val Arg Pro
1 5 10 15

Pro Thr Pro Arg Glu Leu Asp Ser Gln Arg Arg Pro Val Val Gln Val
20 25 30

Val Asp Glu Arg Val Leu Val Phe Asn Pro Glu Glu Pro Asp Gly Gly
35 40 45

Phe Pro Gly Leu Lys Trp Gly Gly Thr His Asp Gly Pro Lys Lys Lys
 50 55 60

Gly Lys Asp Leu Thr Phe Val Phe Asp Arg Val Phe Gly Glu Ala Ala
 65 70 75 80

Thr Gln Gln Asp Val Phe Gln His Thr Thr His Ser Val Leu Asp Ser
 85 90 95

Phe Leu Gln Gly Tyr Asn Cys Ser Val Phe Ala Tyr Gly Ala Thr Gly
 100 105 110

Ala Gly Lys Thr His Thr Met Leu Gly Arg Glu Gly Asp Pro Gly Ile
 115 120 125

Met Tyr Leu Thr Thr Val Glu Leu Tyr Arg Arg Leu Glu Ala Arg Gln
 130 135 140

Gln Glu Lys His Phe Glu Val Leu Ile Ser Tyr Gln Glu Val Tyr Asn
 145 150 155 160

Glu Gln Ile His Asp Leu Leu Glu Pro Lys Gly Pro Leu Ala Ile Arg
 165 170 175

Glu Asp Pro Asp Lys Gly Val Val Gln Gly Leu Ser Phe His Gln
 180 185 190

Pro Ala Ser Ala Glu Gln Leu Leu Glu Ile Leu Thr Arg Gly Asn Arg
 195 200 205

Asn Arg Thr Gln His Pro Thr Asp Ala Asn Ala Thr Ser Ser Arg Ser
 210 215 220

His Ala Ile Phe Gln Ile Phe Val Lys Gln Gln Asp Arg Val Pro Gly
 225 230 235 240

Leu Thr Gln Ala Val Gln Val Ala Lys Met Ser Leu Ile Asp Leu Ala
 245 250 255

Gly Ser Glu Arg Ala Ser Ser Thr His Ala Lys Gly Glu Arg Leu Arg
 260 265 270

Glu Gly Ala Asn Ile Asn Arg Ser Leu Leu Ala Leu Ile Asn Val Leu
 275 280 285

Asn Ala Leu Ala Asp Ala Lys Gly Arg Lys Thr His Val Pro Tyr Arg
 290 295 300

Asp Ser Lys Leu Thr Arg Leu Leu Lys Asp Ser Leu Gly Gly Asn Cys
 305 310 315 320

Arg Thr Val Met Ile Ala Ala Ile Ser Pro Ser Ser Leu Thr Tyr Glu
 325 330 335

Asp Thr Tyr Asn Thr Leu Lys Tyr Ala Asp Arg Ala Lys Glu Ile Arg
 340 345 350

Leu Lys Gly Asn Ser Lys Leu Glu Gly Lys Pro Ile Pro Asn Pro Leu
 355 360 365

Leu Gly Leu Asp Ser Thr Arg Thr Gly His His His His His His His
370 375 380

<210> 6
<211> 1152
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: HsKip3a
fragment

<220>
<223> Nucleotide sequence of HsKip3a fragment used in
ATPase assay (Figure 5).

<400> 6
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gagctggaca gtcagcggcg gccagtggtt cagggtgtgg acgagcgggt gctgggtttt 120
aaccctgagg agcccgtatgg agggttccct ggcctgaaat ggggtggcac ccatgatggc 180
cccaagaaga agggcaaaga cctgacgttt gtcttgacc gggctttgg cgaggcggcc 240
acccaacagg acgtgttcca gcacaccacg cacagcgtcc tggacagctt cctccagggc 300
tacaactgct cagttttgc ctacggggcc accggggctg ggaagacaca caccatgctg 360
ggaaggggagg gggaccccg catcatgtac ctgaccaccg tggaaactgta caggcgcctg 420
gaggcccgcc agcaggagaa gcacttcgag gtgtcatca gctaccagga ggtgtataat 480
gaacagatcc atgaccccttggagcccaag gggcccttg ccatccgcga ggaccccgac 540
aagggggtgg tggtaagg actttcttc caccagccag cctcagccga gcagctgctg 600
gagatactga ccagggggaa ccgtaacccgc acgcagcacc ccactgatgc caacgcgact 660
tcctcccgct cccatccat cttccagatc ttgtgaagc agcaggaccg ggttccagga 720
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gcatcccgca cccatgcgaa gggggagccgg ctgcgggagg gggccaacat caaccgcctt 840
ctgctggcgc tcatcaacgt cctcaatgcc ttggccgatg caaaggcccga caagacccat 900
gtgccttacc gggacagcaa actgacccgc ctgctcaaag actccctcgg gggcaactgc 960
cgcacagtga tgatcgctgc catcagcccc tccagcctga cctacgagga cacgtacaac 1020
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catcaccatt ga 1152